

#3

SEQUENCE LISTING

<110> Anderson, David

<120> METHODS AND COMPOSITIONS COMPRISING RENILLA GFP

Sub 3B
<130> A-68531-1/DJB/RMS/AMS

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<141> 2000-11-10

<150> US 60/164,592

<151> 1999-11-10

<160> 85

<170> PatentIn version 3.0

<210> 1

<211> 1079

<212> DNA

<213> Renilla muelleri

<220>

<221> CDS

<222> (259) .. (975)

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acataatatc taagagacgc ctcattttaag agtagtaaaa atataatata tgatagagta	180
tacaactctc gccttagaca gacagtgtgc aacagagtaa ctcttggttaa tgcaatcgaa	240
agcgtcaaga gagataag atg agt aaa caa ata ttg aag aac act tgt tta	291
Met Ser Lys Gln Ile Leu Lys Asn Thr Cys Leu	
1 5 10	
caa gaa gta atg tcg tat aaa gta aat ctg gaa gga att gta aac aac	339
Gln Glu Val Met Ser Tyr Lys Val Asn Leu Glu Gly Ile Val Asn Asn	
15 20 25	
cat gtt ttt aca atg gag ggt tgc ggc aaa ggg aat att tta ttc ggc	387
His Val Phe Thr Met Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly	
30 35 40	
aat caa ctg gtt cag att cgt gtc acg aaa ggg gcc cca ctg cct ttt	435
Asn Gln Leu Val Gln Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe	
45 50 55	
gca ttt gat att gtg tca cca gct ttt caa tat ggc aac cgt act ttc	483
Ala Phe Asp Ile Val Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe	
60 65 70 75	
acg aaa tat ccg aat gat ata tca gat tat ttt ata caa tca ttt cca	531
Thr Lys Tyr Pro Asn Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro	
80 85 90	
gca gga ttt atg tat gaa cga aca tta cgt tac gaa gat ggc gga ctt	579
Ala Gly Phe Met Tyr Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu	
95 100 105	
gtt gaa att cgt tca gat ata aat tta ata gaa gac aag ttc gtc tac	627
Val Glu Ile Arg Ser Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr	
110 115 120	
aga gtc gaa tac aaa ggt agt aac ttc cca gat gat ggt ccc gtc atg	675
Arg Val Glu Tyr Lys Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met	
125 130 135	

cag aag act atc tta gga ata gag cct tca ttt gaa gcc atg tac atg 723
 Gln Lys Thr Ile Leu Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met
 140 145 150 155

aat aat ggc gtc ttg gtc ggc gaa gta att ctt gtc tat aaa cta aac 771
 Asn Asn Gly Val Leu Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn
 160 165 170

tct ggg aaa tat tat tca tgt cac atg aaa aca tta atg aag tcg aaa 819
 Ser Gly Lys Tyr Tyr Ser Cys His Met Lys Thr Leu Met Lys Ser Lys
 175 180 185

ggc gta gta aag gag ttt cct tcg tat cat ttt att caa cat cgt ttg 867
 Gly Val Val Lys Glu Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu
 190 195 200

gaa aag act tac gta gaa gac ggg ggg ttc gtt gaa cag cat gag act 915
 Glu Lys Thr Tyr Val Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr
 205 210 215

gct att gct caa atg aca tct ata gga aaa cca cta gga tcc tta cac 963
 Ala Ile Ala Gln Met Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His
 220 225 230 235

gaa tgg gtt taa acacagttac attacttttt ccaattcgtg tttcatgtca 1015
 Glu Trp Val

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aaaa 1079

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<213> Renilla muelleri

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Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly Asn Gln Leu Val Gln
 35 40 45

Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val
 50 55 60

Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Asn
 65 70 75 80

Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro Ala Gly Phe Met Tyr
 85 90 95

Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu Val Glu Ile Arg Ser
 100 105 110

Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr Arg Val Glu Tyr Lys
 115 120 125

Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met Gln Lys Thr Ile Leu
 130 135 140

Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met Asn Asn Gly Val Leu
 145 150 155 160

Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn Ser Gly Lys Tyr Tyr
 165 170 175

Ser Cys His Met Lys Thr Leu Met Lys Ser Lys Gly Val Val Lys Glu
 180 185 190

Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu Glu Lys Thr Tyr Val
 195 200 205

Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln Met

210

215

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Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
 225 230 235

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<212> DNA

<213> Ptilosarcus Gurneyi

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cgggttaciaa agggaggtcc gttgccattc gctttcgata ttgtttccat agctttccaa	240
tacgggaatc gcactttcac gaaataccca gacgacattg cggactactt tgttcaatca	300
ttcccggctg gattttttcta cgaaagaaat ctacgctttg aagatggcgc cattgttgac	360
attcggttcag atataagttt agaagatgat aagttccact acaaagtggg gtatagaggc	420
aacgggtttcc ctagtaacgg acccgtgatg caaaaagcca tcctcggcat ggagccatcg	480
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ctcgagtcag ggaactatta ctctgtccac atgaaaacgt ttacagatc caaaggtgga	600
gtgaaagaat tcccgaata tcautttatc catcatcgtc tggagaaaac ctacgtggaa	660
gaaggaagct tcgtggaaca acacgagacg gccattgcac aactgaccac aattggaaaa	720
cctctgggct cccttcatga atgggtgtag aaaatgacca atatactggg gaaaccgata	780
accgttttga agcttgtgta tacaaattat ttgggggtcat tttgtaatgt gtatgtgtgt	840
tgtatgatca atagacgtcg tcattcatag cttgaatcct tcagcaaaag aaacctcgaa	900
gcatattgaa acctcgaagc atattgaaac ctcgacggag agcgtaaaga gaccgcacaa	960

attaacgcgt ttcaaccagc agttggaatc tttaaaccga tcaaaactat taatataaat 1020
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atg tcg gca aaa gct agc gtt gaa gga atc gtg aac aat cac gtt ttt 96
 Met Ser Ala Lys Ala Ser Val Glu Gly Ile Val Asn Asn His Val Phe
 15 20 25 30

tcc atg gaa gga ttt gga aaa ggc aat gta tta ttt gga aac caa ttg 144
 Ser Met Glu Gly Phe Gly Lys Gly Asn Val Leu Phe Gly Asn Gln Leu
 35 40 45

atg caa atc cgg gtt aca aag gga ggt ccg ttg cca ttc gct ttc gac 192
 Met Gln Ile Arg Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp
 50 55 60

att gtt tcc ata gct ttc caa tac ggg aat cgc act ttc acg aaa tac 240
 Ile Val Ser Ile Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr
 65 70 75

cca gac gac att gcg gac tac ttt gtt caa tca ttt ccg gct gga ttt 288
 Pro Asp Asp Ile Ala Asp Tyr Phe Val Gln Ser Phe Pro Ala Gly Phe
 80 85 90

ttc tac gaa aga aat cta cgc ttt gaa gat ggc gcc att gtt gac att	336
Phe Tyr Glu Arg Asn Leu Arg Phe Glu Asp Gly Ala Ile Val Asp Ile	
95 100 105 110	
cgt tca gat ata agt tta gaa gat gat aag ttc cac tac aaa gtg gag	384
Arg Ser Asp Ile Ser Leu Glu Asp Asp Lys Phe His Tyr Lys Val Glu	
115 120 125	
tat aga ggc aac ggt ttc cct agt aac gga ccc gtg atg caa aaa gcc	432
Tyr Arg Gly Asn Gly Phe Pro Ser Asn Gly Pro Val Met Gln Lys Ala	
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atc ctc ggc atg gag cca tcg ttt gag gtg gtc tac atg aac agc ggc	480
Ile Leu Gly Met Glu Pro Ser Phe Glu Val Val Tyr Met Asn Ser Gly	
145 150 155	
gtt ctg gtg ggc gaa gta gat ctc gtt tac aaa ctc gag tca ggg aac	528
Val Leu Val Gly Glu Val Asp Leu Val Tyr Lys Leu Glu Ser Gly Asn	
160 165 170	
tat tac tcg tgc cac atg aaa acg ttt tac aga tcc aaa ggt gga gtg	576
Tyr Tyr Ser Cys His Met Lys Thr Phe Tyr Arg Ser Lys Gly Gly Val	
175 180 185 190	
aaa gaa ttc ccg gaa tat cac ttt atc cat cat cgt ctg gag aaa acc	624
Lys Glu Phe Pro Glu Tyr His Phe Ile His His Arg Leu Glu Lys Thr	
195 200 205	
tac gtg gaa gaa gga agc ttc gtg gaa caa cac gag acg gcc att gca	672
Tyr Val Glu Glu Gly Ser Phe Val Glu Gln His Glu Thr Ala Ile Ala	
210 215 220	
caa ctg acc aca att gga aaa cct ctg ggc tcc ctt cat gaa tgg gtg	720
Gln Leu Thr Thr Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val	
225 230 235	
tagaaaatga ccaatatact ggggaaaatc accaatatac tggggaaaat gaccaattta	780
ctggggaaaa tgaccaatat actgtagaaa atcaccaata tactggggaa aatgaccaat	840
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cgtcgtcatt catagcttga atccttcagc aaaagaaacc tcgaagcata ttgaaacctc	1080
gacggagagc ataaagagac cgcacgtaca caaattataa taccagcagt tggaatcttt	1140

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<212> PRT

<213> Ptilosarcus Gurneyi

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Ala Lys Ala Ser Val Glu Gly Ile Val Asn Asn His Val Phe Ser Met
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Glu Gly Phe Gly Lys Gly Asn Val Leu Phe Gly Asn Gln Leu Met Gln
35 40 45

Ile Arg Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile Val
50 55 60

Ser Ile Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Asp
65 70 75 80

Asp Ile Ala Asp Tyr Phe Val Gln Ser Phe Pro Ala Gly Phe Phe Tyr
85 90 95

Glu Arg Asn Leu Arg Phe Glu Asp Gly Ala Ile Val Asp Ile Arg Ser
100 105 110

Asp Ile Ser Leu Glu Asp Asp Lys Phe His Tyr Lys Val Glu Tyr Arg
115 120 125

Gly Asn Gly Phe Pro Ser Asn Gly Pro Val Met Gln Lys Ala Ile Leu
 130 135 140

Gly Met Glu Pro Ser Phe Glu Val Val Tyr Met Asn Ser Gly Val Leu
 145 150 155 160

Val Gly Glu Val Asp Leu Val Tyr Lys Leu Glu Ser Gly Asn Tyr Tyr
 165 170 175

Ser Cys His Met Lys Thr Phe Tyr Arg Ser Lys Gly Gly Val Lys Glu
 180 185 190

Phe Pro Glu Tyr His Phe Ile His His Arg Leu Glu Lys Thr Tyr Val
 195 200 205

Glu Glu Gly Ser Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln Leu
 210 215 220

Thr Thr Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
 225 230 235

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<211> 238

<212> PRT

<213> Aequorea victoria

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 7

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<212> PRT

<213> Aequorea victoria

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	35	40	45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	50	55	60
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln	65	70	75
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	85	90	95
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	100	105	110
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	115	120	125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	130	135	140
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	145	150	155
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	165	170	175
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro	180	185	190
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser	195	200	205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val	210	215	220
Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	225	230	235

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<223> Consensus sequence

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<222> (7)..(7)

<223> "Xaa" at position 7 can be either Leu or Lys.

<220>

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<222> (8)..(8)

<223> "Xaa" at position 8 can be either Asn or Phe.

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<223> "Xaa" at position 13 can be either Glu or Pro.

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<223> "Xaa" at position 15 can be either Met or Leu.

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<222> (17)..(17)
<223> "Xaa" at position 17 can be either Ala or Tyr.

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<223> "Xaa" at position 22 can be either Glu or Asp.

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<223> "Xaa" at position 24 can be either Ile or Asp.

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<223> "Xaa" at position 27 can be either Gly or Asn.

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<223> "Xaa" at position 29 can be either Val or Lys.

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<222> (32)..(32)
<223> "Xaa" at position 32 can be either Val or Met.

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<223> "Xaa" at position 33 can be either Ser or Glu.

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<223> "Xaa" at position 37 can be either Lys or Glu.

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<223> "Xaa" at position 39 can be either Asn or Asp.

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<223> "Xaa" at position 42 can be either Phe or Tyr.

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<223> "Xaa" at position 44 can be either Asn or Lys.

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<222> (45)..(45)
<223> "Xaa" at position 45 can be either Gln or Leu.

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<223> "Xaa" at position 46 can be either Thr or Leu.

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<223> "Xaa" at position 48 can be either Gln or Lys.

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<223> "Xaa" at position 63 can be either Ile or Thr.

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<223> "Xaa" at position 67 can be either Ala or Thr.

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<223> "Xaa" at position 74 can be either Thr or Cys.

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<223> "Xaa" at position 77 can be either Lys or Arg.

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<223> "Xaa" at position 83 can be either Tyr or Phe.

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<223> "Xaa" at position 98 can be either Gln or Tyr.

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<223> "Xaa" at position 102 can be either Ile or Leu.

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<222> (142)..(142)
<223> "Xaa" at position 142 can be either Gln or Gly.

<220>

<221> SITE
<222> (143)..(143)
<223> "Xaa" at position 143 can be either Lys or His.

<220>
<221> SITE
<222> (145)..(145)
<223> "Xaa" at position 145 can be either Leu or Ile.

<220>
<221> SITE
<222> (146)..(146)
<223> "Xaa" at position 146 can be either Leu or Glu.

<220>
<221> SITE
<222> (147)..(147)
<223> "Xaa" at position 147 can be either Gly or Tyr.

<220>
<221> SITE
<222> (149)..(149)
<223> "Xaa" at position 149 can be either Glu or Tyr.

<220>

<221> SITE
<222> (150)..(150)
<223> "Xaa" at position 150 can be either Pro or Asn.

<220>
<221> SITE
<222> (152)..(152)
<223> "Xaa" at position 152 can be either His or Phe.

<220>
<221> SITE
<222> (153)..(153)
<223> "Xaa" at position 153 can be either Asn or Glu.

<220>
<221> SITE
<222> (156)..(156)
<223> "Xaa" at position 156 can be either Tyr or Ile.

<220>
<221> SITE
<222> (158)..(158)
<223> "Xaa" at position 158 can be either Asn or Ala.

<220>

<221> SITE
<222> (165)..(165)
<223> "Xaa" at position 165 can be either Val or Ile.

<220>
<221> SITE
<222> (166)..(166)
<223> "Xaa" at position 166 can be either Lys or Leu.

<220>
<221> SITE
<222> (168)..(168)
<223> "Xaa" at position 168 can be either Gly or Asn.

<220>
<221> SITE
<222> (169)..(169)
<223> "Xaa" at position 169 can be either Glu or Phe.

<220>
<221> SITE
<222> (170)..(170)
<223> "Xaa" at position 170 can be either Lys or Val.

<220>

<221> SITE
<222> (172) .. (172)
<223> "Xaa" at position 172 can be either Leu or Arg.

<220>
<221> SITE
<222> (173) .. (173)
<223> "Xaa" at position 173 can be either Val or His.

<220>
<221> SITE
<222> (174) .. (174)
<223> "Xaa" at position 174 can be either Asn or Tyr.

<220>
<221> SITE
<222> (175) .. (175)
<223> "Xaa" at position 175 can be either Lys or Ile.

<220>
<221> SITE
<222> (176) .. (176)
<223> "Xaa" at position 176 can be either Leu or Glu.

<220>

<221> SITE
<222> (178)..(179)
<223> "Xaa" at positions 178-179 can be either Ser or Gly.

<220>
<221> SITE
<222> (181)..(181)
<223> "Xaa" at position 181 can be either Tyr or Gln.

<220>
<221> SITE
<222> (182)..(182)
<223> "Xaa" at position 182 can be either Tyr or Glu.

<220>
<221> SITE
<222> (183)..(183)
<223> "Xaa" at position 183 can be either Ser or Ala.

<220>
<221> SITE
<222> (184)..(184)
<223> "Xaa" at position 184 can be either Cys or Asp.

<220>

<221> SITE
<222> (186)..(186)
<223> "Xaa" at position 186 can be either Met or Tyr.

<220>
<221> SITE
<222> (187)..(187)
<223> "Xaa" at position 187 can be either Lys or Gln.

<220>
<221> SITE
<222> (188)..(188)
<223> "Xaa" at position 188 can be either Thr or Gln.

<220>
<221> SITE
<222> (192)..(192)
<223> "Xaa" at position 192 can be either Ser or Ile.

<220>
<221> SITE
<222> (193)..(193)
<223> "Xaa" at position 193 can be either Lys or Gly.

<220>

<221> SITE
<222> (194)..(194)
<223> "Xaa" at position 194 can be either Asp or Gly.

<220>
<221> SITE
<222> (196)..(196)
<223> "Xaa" at position 196 can be either Val or Pro.

<220>
<221> SITE
<222> (197)..(197)
<223> "Xaa" at position 197 can be either Val or Lys.

<220>
<221> SITE
<222> (198)..(198)
<223> "Xaa" at position 198 can be either Glu or Leu.

<220>
<221> SITE
<222> (199)..(199)
<223> "Xaa" at position 199 can be either Phe or Leu.

<220>

<221> SITE
<222> (202)..(202)
<223> "Xaa" at position 202 can be either Tyr or Asn.

<220>
<221> SITE
<222> (204)..(204)
<223> "Xaa" at position 204 can be either Phe or Tyr.

<220>
<221> SITE
<222> (205)..(205)
<223> "Xaa" at position 205 can be either Ile or Leu.

<220>
<221> SITE
<222> (209)..(209)
<223> "Xaa" at position 209 can be either Thr or Leu.

<220>
<221> SITE
<222> (210)..(210)
<223> "Xaa" at position 210 can be either Glu or Gln.

<220>

<221> SITE
<222> (211)..(211)
<223> "Xaa" at position 211 can be either Ser or Lys.

<220>
<221> SITE
<222> (212)..(212)
<223> "Xaa" at position 212 can be either Thr or Ala.

<220>
<221> SITE
<222> (213)..(213)
<223> "Xaa" at position 213 can be either Tyr or Leu.

<220>
<221> SITE
<222> (214)..(214)
<223> "Xaa" at position 214 can be either Val or Ser.

<220>
<221> SITE
<222> (215)..(215)
<223> "Xaa" at position 215 can be either Glu or Lys.

<220>

<221> SITE
<222> (217)..(217)
<223> "Xaa" at position 217 can be either Gly or Pro.

<220>
<221> SITE
<222> (219)..(219)
<223> "Xaa" at position 219 can be either Phe or Glu.

<220>
<221> SITE
<222> (220)..(220)
<223> "Xaa" at position 220 can be either Val or Lys.

<220>
<221> SITE
<222> (221)..(221)
<223> "Xaa" at position 221 can be either Glu or Arg.

<220>
<221> SITE
<222> (222)..(222)
<223> "Xaa" at position 222 can be either Gln or Asp.

<220>

<221> SITE
<222> (224)..(224)
<223> "Xaa" at position 222 can be either Glu or Met.

<220>
<221> SITE
<222> (225)..(225)
<223> "Xaa" at position 225 can be either Thr or Val.

<220>
<221> SITE
<222> (226)..(226)
<223> "Xaa" at position 226 can be either Ala or Leu.

<220>
<221> SITE
<222> (227)..(227)
<223> "Xaa" at position 227 can be either Ile or Leu.

<220>
<221> SITE
<222> (228)..(228)
<223> "Xaa" at position 228 can be either Ala or Glu.

<220>

<221> SITE
<222> (229)..(229)
<223> "Xaa" at position 229 can be either Gln or Phe.

<220>
<221> SITE
<222> (233)..(233)
<223> "Xaa" at position 233 can be either Ile or Ala.

<220>
<221> SITE
<222> (235)..(235)
<223> "Xaa" at position 235 can be either Ile or Lys.

<220>
<221> SITE
<222> (236)..(236)
<223> "Xaa" at position 236 can be either Pro or Tyr.

<220>
<221> SITE
<222> (239)..(239)
<223> "Xaa" at position 239 can be either Ser or Met.

<220>

<221> SITE
<222> (240) .. (240)
<223> "Xaa" at position 240 can be either Leu or Asp.

<220>
<221> SITE
<222> (241) .. (241)
<223> "Xaa" at position 241 can be either Glu or His.

<220>
<221> SITE
<222> (242) .. (242)
<223> "Xaa" at position 242 can be either Glu or Leu.

<220>
<221> SITE
<222> (243) .. (243)
<223> "Xaa" at position 243 can be either Trp or Tyr.

<220>
<221> SITE
<222> (244) .. (244)
<223> "Xaa" at position 244 can be either Val or Lys.

<400> 8

<211> 61

<212> PRT

<213> Artificial

<220>

<223> coiled coil structure

<400> 9

Met	Gly	Cys	Ala	Ala	Leu	Glu	Ser	Glu	Val	Ser	Ala	Leu	Glu	Ser	Glu
1				5					10					15	

Val	Ala	Ser	Leu	Glu	Ser	Glu	Val	Ala	Ala	Leu	Gly	Arg	Gly	Asp	Met
			20					25						30	

Pro	Leu	Ala	Ala	Val	Lys	Ser	Lys	Leu	Ser	Ala	Val	Lys	Ser	Lys	Leu
		35					40						45		

Ala	Ser	Val	Lys	Ser	Lys	Leu	Ala	Ala	Cys	Gly	Pro	Pro
	50					55					60	

<210> 10

<211> 6

<212> PRT

<213> Artificial

<220>

<223> loop structure

<400> 10

Gly	Arg	Gly	Asp	Met	Pro
1				5	

<210> 11

<211> 69

<212> PRT

<213> Artificial

<220>

<223> minibody presentation structure

<400> 11

Met Gly Arg Asn Ser Gln Ala Thr Ser Gly Phe Thr Phe Ser His Phe
1 5 10 15

Tyr Met Glu Trp Val Arg Gly Gly Glu Tyr Ile Ala Ala Ser Arg His
20 25 30

Lys His Asn Lys Tyr Thr Thr Glu Tyr Ser Ala Ser Val Lys Gly Arg
35 40 45

Tyr Ile Val Ser Arg Asp Thr Ser Gln Ser Ile Leu Tyr Leu Gln Lys
50 55 60

Lys Lys Gly Pro Pro
65

<210> 12

<211> 14

<212> PRT

<213> Artificial

<220>

<223> Preferred C2H2 zinc finger sequence

<220>

<221> UNSURE

<222> (7)..(7)

<223> "Xaa" at position 7 is a random peptide of any 3 to 20 amino acid

<400> 12

Phe Gln Cys Glu Glu Cys Xaa His Ile Arg Ser His Thr Gly
1 5 10

<210> 13

<211> 14

<212> PRT

<213> Artificial

<220>

<223> Preferred CCHC box based on nucleocapsid protein P2

<220>

<221> UNSURE

<222> (7)..(7)

<223> "Xaa" at position 7 can be any 4 to 20 amino acids.

<400> 13

Val Lys Cys Phe Asn Cys Xaa His Thr Ala Arg Asn Cys Arg
1 5 10

<210> 14

<211> 15

<212> PRT

<213> Artificial

<220>

<223> Preferred CCHC box based on the nmr structural ensemble 1ZFP.

<220>

<221> UNSURE

<222> (10)..(10)

<223> "Xaa" at position 10 can be any 4 to 20 amino acids.

<400> 14

Met	Asn	Pro	Asn	Cys	Ala	Arg	Cys	Gly	Xaa	His	Lys	Ala	Cys	Phe
1				5					10					15

<210> 15

<211> 7

<212> PRT

<213> Artificial

<220>

<223> dimerization sequence

<400> 15

Glu	Phe	Leu	Ile	Val	Lys	Ser
1				5		

<210> 16

<211> 9

<212> PRT

<213> Artificial

<220>

<223> dimerization sequence

<400> 16

Glu Glu Phe Leu Ile Val Lys Lys Ser
1 5

<210> 17

<211> 7

<212> PRT

<213> Artificial

<220>

<223> dimerization sequence

<400> 17

Phe Glu Ser Ile Lys Leu Val
1 5

<210> 18

<211> 7

<212> PRT

<213> Artificial

<220>

<223> dimerization sequence

<400> 18

Val Ser Ile Lys Phe Glu Leu
1 5

<210> 19

<211> 7

<212> PRT

<213> Simian virus 40

<400> 19

Pro Lys Lys Lys Arg Lys Val
1 5

<210> 20

<211> 6

<212> PRT

<213> Homo sapiens

<400> 20

Ala Arg Arg Arg Arg Pro
1 5

<210> 21

<211> 10

<212> PRT

<213> Mus musculus

<400> 21

Glu Glu Val Gln Arg Lys Arg Gln Lys Leu
1 5 10

<210> 22

<211> 9

<212> PRT

<213> Mus musculus

<400> 22

Glu Glu Lys Arg Lys Arg Thr Tyr Glu

1 5

<210> 23

<211> 20

<212> PRT

<213> *Xenopus laevis*

<400> 23

Ala Val Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys
1 5 10 15

Lys Lys Leu Asp
20

<210> 24

<211> 31

<212> PRT

<213> *Mus musculus*

<400> 24

Met Ala Ser Pro Leu Thr Arg Phe Leu Ser Leu Asn Leu Leu Leu Leu
1 5 10 15

Gly Glu Ser Ile Leu Gly Ser Gly Glu Ala Lys Pro Gln Ala Pro
20 25 30

<210> 25

<211> 21

<212> PRT

<213> *Homo sapiens*

<400> 25

Met Ser Ser Phe Gly Tyr Arg Thr Leu Thr Val Ala Leu Phe Thr Leu
 1 5 10 15

Ile Cys Cys Pro Gly
 20

<210> 26

<211> 51

<212> PRT

<213> Mus musculus

<400> 26

Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly Ser Val Lys Gly Thr
 1 5 10 15

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
 20 25 30

Ile Cys Val Ala Leu Leu Leu Ser Leu Ile Ile Thr Leu Ile Cys Tyr
 35 40 45

His Ser Arg
 50

<210> 27

<211> 33

<212> PRT

<213> Homo sapiens

<400> 27

Met Val Ile Ile Val Thr Val Val Ser Val Leu Leu Ser Leu Phe Val
 1 5 10 15

Thr Ser Val Leu Leu Cys Phe Ile Phe Gly Gln His Leu Arg Gln Gln
 20 25 30

Arg

<210> 28

<211> 37

<212> PRT

<213> Rattus sp.

<400> 28

Pro	Asn	Lys	Gly	Ser	Gly	Thr	Thr	Ser	Gly	Thr	Thr	Arg	Leu	Leu	Ser
1				5					10					15	

Gly	His	Thr	Cys	Phe	Thr	Leu	Thr	Gly	Leu	Leu	Gly	Thr	Leu	Val	Thr
			20					25					30		

Met	Gly	Leu	Leu	Thr
			35	

<210> 29

<211> 14

<212> PRT

<213> Homo sapiens

<400> 29

Met	Gly	Ser	Ser	Lys	Ser	Lys	Pro	Lys	Asp	Pro	Ser	Gln	Arg
1				5					10				

<210> 30

<211> 26

<212> PRT

<213> Homo sapiens

<400> 30

Leu Leu Gln Arg Leu Phe Ser Arg Gln Asp Cys Cys Gly Asn Cys Ser
 1 5 10 15

Asp Ser Glu Glu Glu Leu Pro Thr Arg Leu
 20 25

<210> 31

<211> 20

<212> PRT

<213> Rattus norvegicus

<400> 31

Lys Gln Phe Arg Asn Cys Met Leu Thr Ser Leu Cys Cys Gly Lys Asn
 1 5 10 15

Pro Leu Gly Asp
 20

<210> 32

<211> 19

<212> PRT

<213> Homo sapiens

<400> 32

Leu Asn Pro Pro Asp Glu Ser Gly Pro Gly Cys Met Ser Cys Lys Cys
 1 5 10 15

Val Leu Ser

<210> 33

<211> 5

<212> PRT

<213> Artificial

<220>

<223> lysomal degradation sequence

<400> 33

Lys Phe Glu Arg Gln
1 5

<210> 34

<211> 36

<212> PRT

<213> Cricetulus griseus

<400> 34

Met Leu Ile Pro Ile Ala Gly Phe Phe Ala Leu Ala Gly Leu Val Leu
1 5 10 15
Ile Val Leu Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser His Ala Gly
20 25 30
Tyr Gln Thr Ile
35

<210> 35

<211> 35

<212> PRT

<213> Homo sapiens

<400> 35

Leu Val Pro Ile Ala Val Gly Ala Ala Leu Ala Gly Val Leu Ile Leu
1 5 10 15
Val Leu Leu Ala Tyr Phe Ile Gly Leu Lys His His His Ala Gly Tyr
20 25 30

Glu Gln Phe
35

<210> 36

<211> 27

<212> PRT

<213> yeast

<400> 36

Met Leu Arg Thr Ser Ser Leu Phe Thr Arg Arg Val Gln Pro Ser Leu
1 5 10 15

Phe Ser Arg Asn Ile Leu Arg Leu Gln Ser Thr
20 25

<210> 37

<211> 25

<212> PRT

<213> yeast

<400> 37

Met Leu Ser Leu Arg Gln Ser Ile Arg Phe Phe Lys Pro Ala Thr Arg
1 5 10 15

Thr Leu Cys Ser Ser Arg Tyr Leu Leu
20 25

<210> 38

<211> 64

<212> PRT

<213> yeast

<400> 38

Met	Phe	Ser	Met	Leu	Ser	Lys	Arg	Trp	Ala	Gln	Arg	Thr	Leu	Ser	Lys
1				5					10					15	
Ser	Phe	Tyr	Ser	Thr	Ala	Thr	Gly	Ala	Ala	Ser	Lys	Ser	Gly	Lys	Leu
			20				25						30		
Thr	Gln	Lys	Leu	Val	Thr	Ala	Gly	Val	Ala	Ala	Ala	Gly	Ile	Thr	Ala
		35					40					45			
Ser	Thr	Leu	Leu	Tyr	Ala	Asp	Ser	Leu	Thr	Ala	Glu	Ala	Met	Thr	Ala
	50					55					60				

<210> 39

<211> 41

<212> PRT

<213> yeast

<400> 39

Met	Lys	Ser	Phe	Ile	Thr	Arg	Asn	Lys	Thr	Ala	Ile	Leu	Ala	Thr	Val
1				5					10					15	
Ala	Ala	Thr	Gly	Thr	Ala	Ile	Gly	Ala	Tyr	Tyr	Tyr	Tyr	Asn	Gln	Leu
			20				25						30		
Gln	Gln	Gln	Gln	Gln	Arg	Gly	Lys	Lys							
		35				40									

<210> 40

<211> 4

<212> PRT

<213> Artificial

<220>

<223> endoplasmic reticulum sequence

<400> 40

Lys Asp Glu Leu
1

<210> 41

<211> 15

<212> PRT

<213> adenovirus

<400> 41

Leu Tyr Leu Ser Arg Arg Ser Phe Ile Asp Glu Lys Lys Met Pro
1 5 10 15

<210> 42

<211> 19

<212> PRT

<213> Mus sp.

<400> 42

Leu Asn Pro Pro Asp Glu Ser Gly Pro Gly Cys Met Ser Cys Lys Cys
1 5 10 15

Val Leu Ser

<210> 43

<211> 15

<212> PRT

<213> Homo sapiens

<400> 43

Leu Thr Glu Pro Thr Gln Pro Thr Arg Asn Gln Cys Cys Ser Asn
 1 5 10 15

<210> 44

<211> 9

<212> PRT

<213> Homo sapiens

<400> 44

Arg Thr Ala Leu Gly Asp Ile Gly Asn
 1 5

<210> 45

<211> 20

<212> PRT

<213> Homo sapiens

<400> 45

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
 1 5 10 15

Val Thr Asn Ser
 20

<210> 46

<211> 29

<212> PRT

<213> Homo sapiens

<400> 46

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu

1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr
20 25

<210> 47

<211> 27

<212> PRT

<213> Homo sapiens

<400> 47

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
1 5 10 15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn
20 25

<210> 48

<211> 18

<212> PRT

<213> Influenza virus

<400> 48

Met Lys Ala Lys Leu Leu Val Leu Leu Tyr Ala Phe Val Ala Gly Asp
1 5 10 15

Gln Ile

<210> 49

<211> 24

<212> PRT

<213> Homo sapiens

<400> 49

Met Gly Leu Thr Ser Gln Leu Leu Pro Pro Leu Phe Phe Leu Leu Ala
1 5 10 15

Cys Ala Gly Asn Phe Val His Gly
20

<210> 50

<211> 6

<212> PRT

<213> Artificial

<220>

<223> purification sequence

<400> 50

His His His His His His
1 5

<210> 51

<211> 7

<212> PRT

<213> Artificial

<220>

<223> stability sequence

<220>

<221> UNSURE

<222> (3) .. (3)

<223> "Xaa" at postion 3 is a peptide having at least 4 residues of any

amino acid

<400> 51

Met Gly Xaa Gly Gly Pro Pro
1 5

<210> 52

<211> 5

<212> PRT

<213> Artificial

<220>

<223> linker sequence

<400> 52

Gly Ser Gly Gly Ser
1 5

<210> 53

<211> 4

<212> PRT

<213> Artificial

<220>

<223> linker sequence

<400> 53

Gly Gly Gly Ser
1

<210> 54

<211> 9

<212> PRT

<213> *Xenopus laevis*

<400> 54

Arg Thr Val Leu Gly Val Ile Gly Asp
1 5

<210> 55

<211> 9

<212> PRT

<213> *Homo sapiens*

<400> 55

Arg Thr Ala Leu Gly Ile Asp Gly Asn
1 5

<210> 56

<211> 27

<212> PRT

<213> *Rattus sp.*

<400> 56

Tyr Met Thr Val Ser Ile Ile Asp Arg Phe Met Gln Asp Ser Cys Val
1 5 10 15

Pro Lys Lys Met Leu Gln Leu Val Gly Val Thr
20 25

<210> 57

<211> 28

<212> PRT

<213> Mus sp.

<400> 57

Lys	Phe	Arg	Leu	Leu	Gln	Glu	Thr	Met	Tyr	Met	Thr	Val	Ser	Ile	Ile
1				5					10					15	

Asp	Arg	Phe	Met	Gln	Asn	Ser	Cys	Val	Pro	Lys	Lys
			20					25			

<210> 58

<211> 27

<212> PRT

<213> Mus sp.

<400> 58

Arg	Ala	Ile	Leu	Ile	Asp	Trp	Leu	Ile	Gln	Val	Gln	Met	Lys	Phe	Arg
1				5					10					15	

Leu	Leu	Gln	Glu	Thr	Met	Tyr	Met	Thr	Val	Ser
			20					25		

<210> 59

<211> 27

<212> PRT

<213> Mus sp.

<400> 59

Asp	Arg	Phe	Leu	Gln	Ala	Gln	Leu	Val	Cys	Arg	Lys	Lys	Leu	Gln	Val
1				5					10					15	

Val	Gly	Ile	Thr	Ala	Leu	Leu	Leu	Ala	Ser	Lys
			20					25		

<210> 60

<211> 18

<212> PRT

<213> Mus sp.

<400> 60

Met Ser Val Leu Arg Gly Lys Leu Gln Leu Val Gly Thr Ala Ala Met
1 5 10 15

Leu Leu

<210> 61

<211> 6

<212> PRT

<213> Artificial

<220>

<223> synthetic

<400> 61

Glu Glu Ala Ala Lys Ala
1 5

<210> 62

<211> 55

<212> DNA

<213> Artificial

<220>

<223> synthetic

<400> 62

gatcatagaa ttgccacca tgggcagcaa gcagatcctg aagaacacct gcctg 55

<210> 63

<211> 55

<212> DNA

<213> Artificial

<220>

<223> synthetic primer

<400> 63

gatcatagaa ttgccacca tgggcaaccg caacgtgctg aagaacaccg gcctg 55

<210> 64

<211> 53

<212> DNA

<213> Artificial

<220>

<223> synthetic primer

<400> 64

atgatcgcg cgcctacacc cactcgtgca gggatcccag gggcttgccg atg 53

<210> 65

<211> 83

<212> DNA

<213> Artificial

<220>

<223> synthetic primer

<400> 65

gatccctgca cgagtgggtg gaggaggccg ccaaggccga ctacaaggac gacgacgaca 60

agtaggcccg tgaggcccta agc 83

<210> 66

<211> 80

<212> DNA

<213> Artificial

<220>

<223> synthetic primer

<400> 66

ggccgcttag ggcctcacgg gcctacttgt cgtegtcctt gtagtcggcc ttggcggcct 60

cctccaccca ctcgtagcagg 80

<210> 67

<211> 42

<212> DNA

<213> Artificial

<220>

<223> synthetic primer

<400> 67

gatcatgaat tcgccatgag taaacaaata ttgaagaaca ct 42

<210> 68

<211> 44

<212> DNA

<213> Artificial

<220>

<223> synthetic primer

<400> 68

tagatcgcg cgccttaaac ccattcgtgt aaggatccta gtgg

44

<210> 69

<211> 69

<212> DNA

<213> Artificial

<220>

<223> synthetic primer

<400> 69

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Pro Leu Gly Ser Glu Phe
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Gly Pro Leu Gly Ser
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